



Promiscuous Yet Specific

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Promiscuous yet specific: a methionine-aromatics interaction drives the reaction scope of the family 1 glycosyltransferase *GmUGT88E3* from soybean.

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Supporting Information Placeholder [MM plots, NMR spectra, HPLC chromatograms, MD snapshots]

ABSTRACT: Family 1 glycosyltransferases (GT1s, UGTs) catalyze the regioselective glycosylation of natural products in a single step. We identified *GmUGT88E3* as a particularly promising biocatalyst, able to produce a variety of pure, single glycosidic products from polyphenols with high chemical yields. We investigated this particularly desirable duality towards specificity, *i.e.*, promiscuous towards acceptors while regiospecific. Using high-field NMR, kinetic characterization, molecular dynamics simulations and mutagenesis studies, we uncovered that the main molecular determinant of *GmUGT88E3* specificity is a methionine-aromatic bridge, an interaction often present in protein structures but never reported for enzyme-substrate interactions. Here, mutating Met127 led to inactive proteins or 100-fold reduced activity.

Glycosides are ubiquitous in nature, yet comparatively absent from our human-made chemosphere. Indeed, traditional chemistry struggles with glycosylation reactions, requiring multistep synthesis to ensure control of both regio- and stereoselectivity, resulting in high costs and poor atom economy. Conversely, inverting glycosyltransferases are generally able to catalyze the synthesis of glycosides in a single step from unprotected acceptors.¹ Among those, family 1 glycosyltransferases (GT1s, according to the CAZY database classification),² are of particular biotechnological interest.^{3–7}

GT1s are phylogenetically related and present a GT-B fold, with an active side cleft at the interface of the two Rossmann domains.⁸ GT1s catalyze inverting reactions using UDP- α -D-glucose as donors (hence they are also commonly termed UDP-dependent glycosyltransferases or UGTs), resulting in β -glycosides. Most of them act via base catalysis with a His-Asp dyad as catalytic residues (Figure 1).⁹

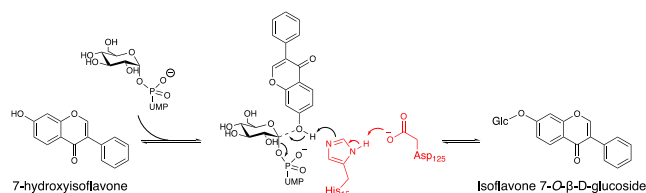


Figure 1. Generalized reaction mechanism for family 1 glycosyltransferases.

Recently, in an effort to develop a predictor for GT1 acceptor selectivity, we assessed reactions catalyzed by 40 GT1s against 32 polyphenol acceptors.¹⁰ Analyzing this dataset, we here identify a high-performing enzyme, *GmUGT88E3*, which showed great activity (>90% conversion in 24 hours) towards 15/32 acceptors with strict regiospecificity on 7 of those 15. Additionally, when assessing yields above 50% in the same timeframe, it presents strict regiospecificity on 14/32 acceptors. Interestingly, *GmUGT88E3* thus appeared to be the most promiscuous enzyme relative to acceptor specificity, while presenting the strictest regiospecificity of all 40 assayed enzymes, two properties that seem opposite. Moreover, while a large number of GT1s present scalability issues related to chemostability, *GmUGT88E3* seemed to be unaffected by the process.¹¹ Overall, *GmUGT88E3* appears to be a very promising biocatalyst for the biotechnological chemosynthesis of polyphenols glucosides. Here, we determine the kinetic parameters of these glycosylation reactions and the NMR structures of the products. Then we used molecular dynamics simulations of the Michaelis complexes and mutagenesis studies to identify the molecular determinants of these unusual properties, uncovering that Met127 is forming a methionine-aromatics bridge (Met-Ar) between Phe126 and the polyphenol acceptors. Strikingly, while Met-Ar interactions have been reported as a common feature involved in protein folding and stability,¹² it has never been described in enzyme-substrate interactions.

GmUGT88E3 has been previously investigated. In a study carried out by Livingstone *et al.* on the transcript levels of six isoflavone 7-O-glucosyltransferases, *GmUGT88E3* (*GmUGT1/GmIF7GT*) transcript levels were found to be significantly higher in early and late seed tissues than the other five GTs¹³. *GmUGT88E3* displays activity towards genistein and daidzein, as was shown by Noguchi

et al.,¹⁴ resulting in the major forms of isoflavones found in soybeans, genistin and daidzin.¹⁵ Though kinetic analysis and structure determination are reported only for genistein, daidzein, and kaempferol, *GmUGT88E3* has been described to show activity towards a wide range of acceptors; flavones, flavanones, flavonols, an aurone, a coumarin and a chalcone.^{14,16}

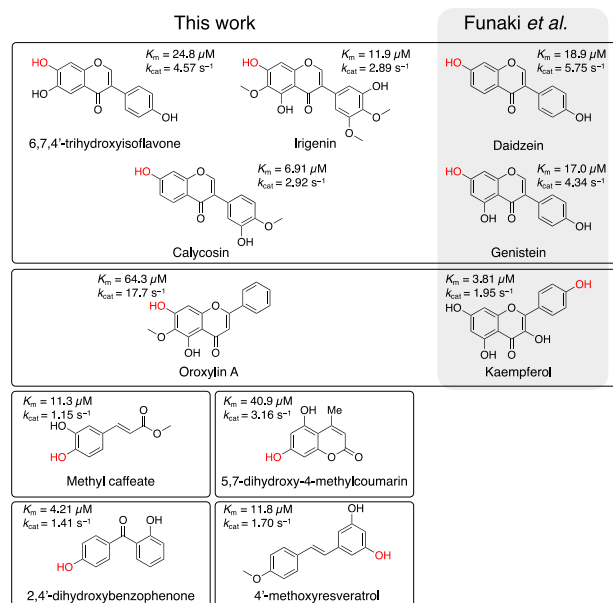


Figure 2. Substrate panel used in this study accompanied by Michaelis-Menten kinetic parameters and the site of glycosylation highlighted in red as uncovered by NMR. Substrates and kinetic parameters as determined by Funaki *et al.* (2015)¹⁶

Thus, we undertook the characterization of the reactions and products of *GmUGT88E3* against 8 polyphenols. The assessed acceptors include three isoflavones, a flavone, methyl caffeate, a coumarin, a benzophenone, and a stilbene demonstrating the promiscuity of the enzyme. *GmUGT88E3* proved to maintain a similar level of specificity and activity over the various assayed chemicals, with k_{cat} in the per-second range (1.15–17.7 s⁻¹) and K_m in the micromolar range (4.21–64.3 μ M) (Figure 2, Table 1).

Table 1. Michaelis-Menten parameters for the aglycones with *GmUGT88E3*

Name	K_m (μ M)	k_{cat} (s ⁻¹)
6,7,4'-trihydroxyisoflavone ^a	24.8 \pm 3.9	4.57 \pm 0.23
Iridenin ^a	11.9 \pm 1.3	2.89 \pm 0.08
Calycosin ^a	6.91 \pm 1.4	2.92 \pm 0.13
Oroxylin A ^a	64.3 \pm 24.2	17.7 \pm 2.71
Methyl caffeate ^a	11.3 \pm 1.3	1.15 \pm 0.03
5,7-dihydroxy-4-methylcoumarin ^a	40.9 \pm 4.7	3.16 \pm 0.13
2,4'-dihydroxybenzophenone ^a	4.21 \pm 1.57	1.41 \pm 0.1
4'-methoxyresveratrol ^a	11.8 \pm 1.18	1.70 \pm 0.04
Kaempferol ^b	3.81 \pm 0.63	1.95 \pm 1.01
Daidzein ^b	18.9 \pm 2.4	5.75 \pm 0.47
Genistein ^b	17.0 \pm 2.3	4.34 \pm 0.6

^aKinetic parameters determined in this study at 20°C and pH 8.0 with 500 μ M UDP-Glc. ^bKinetic parameters as described by Funaki *et al* at 30°C and pH 8.5 with 200 μ M UDP-Glc¹⁶

The site of glycosylation highlighted in red was unraveled by NMR spectroscopy (Figs. S3–S8). The reaction mixture that contained product glycoside, UDP, UDP-glucose, and potentially remaining aglycone was lyophilized, dissolved in DMSO-*d*₆ and directly analyzed by NMR. Glycoside structures of 2,4'-dihydroxybenzophenone and calycosin were determined according to a change in chemical shift of nearby aromatic protons. The sites of glycosylation for the other compounds were identified by 1D NOESY experiments. A response of the nearest aromatic protons was observed through targeted irradiation of the anomeric alpha proton of the resulting glycoside.

GmUGT88E3 is reported as an isoflavone-7-*O*-glycosyltransferase, we observed glycosylation at the 7-position for our assayed isoflavones, as well as glycosylation at the 7-position for the flavone Oroxylin A. On the contrary, kaempferol, a flavone, was glycosylated at the 4'-position as was reported by Funaki *et al.* which raises the hypothesis that in absence of a hydroxide group at the 4'-position, the hydroxide on the 7-position is preferred. Both methyl caffeate and 2,4'-dihydroxybenzophenone are glycosylated at the para position of the aromatic ring. The structure of the 4'-methoxyresveratrol was not determined by NMR since the hydroxides are chemically identical due to free rotation.

In order to establish a better understanding of the determinants governing the broad substrate range of *GmUGT88E3*, molecular dynamics (MD) simulations of the ternary complexes enzyme:UDP-Glc:acceptor were carried out (Figures 3 and S9–S17). The structural model for *GmUGT88E3* was generated using AlphaFold, and the glycosyl donor UDP-Glc was added based on the crystal structure of UGT1 from *P. tinctoria* (PDB 6SU6).¹⁷ The different acceptors were then docked using gnina on this secondary complex.¹⁸ Affinities computed for the 8 aglycones towards the secondary complex UGT:UDP-Glc using the PRODIGY webserver ranged between -7.7 to -9.6 kcal·mol⁻¹ (Table S1),¹⁹ which is on the higher end for enzyme:substrates affinities for transferases (generic average of -5.8 kcal·mol⁻¹).²⁰ Note that these cannot be directly compared to K_m values, as those result from terms related to both affinity and catalysis. Overall, five amino residues have been identified that form important interactions with the aglycones. First, the catalytic base His15, directed by Asp125, forms a hydrogen bond with the reactive hydroxyl. The only other key residue that appears to interact with all compounds is Met127. While rarely described as a key interactor, methionine is known to interact with aromatic amino acids as a stabilizing binding motif.¹² Recently, Weber and Warren carried out a bioinformatics study of all protein structures available in the Protein Data Bank and reported that about 70% of those structures contain a Methionine-aromatic (Met-Ar) interaction and 40% contain a Met-Ar bridge, *i.e.* two aromatics residues interacting via a single methionine. In these bridging interactions, the sulfur is enclosed by two rings from aromatic amino acids.²¹ S-aromatic interactions are reported to occur at 4.5–7 Å, associated with energies comparable to a salt bridge.²² In all our simulations (Figures 3 and S3–S10) we observed a similar interaction, here between the various polyphenol acceptors, Met127, and Phe126, all at distances most frequently described in structural studies. Note that these three residues are consecutive: Asp125, Phe126, and Met127. In addition, Thr155 appears to interact with hydroxides on the opposite side of the glycosylated position in isoflavones. Interestingly, Oroxylin A which is devoid of such a hydroxyl group presents a significantly higher K_m value (Figure 2). Moreover, for 2,4'-dihydroxybenzophenone we observe a strong interaction between Glu197 and the hydroxide on the 4-position, which might explain its low K_m value.

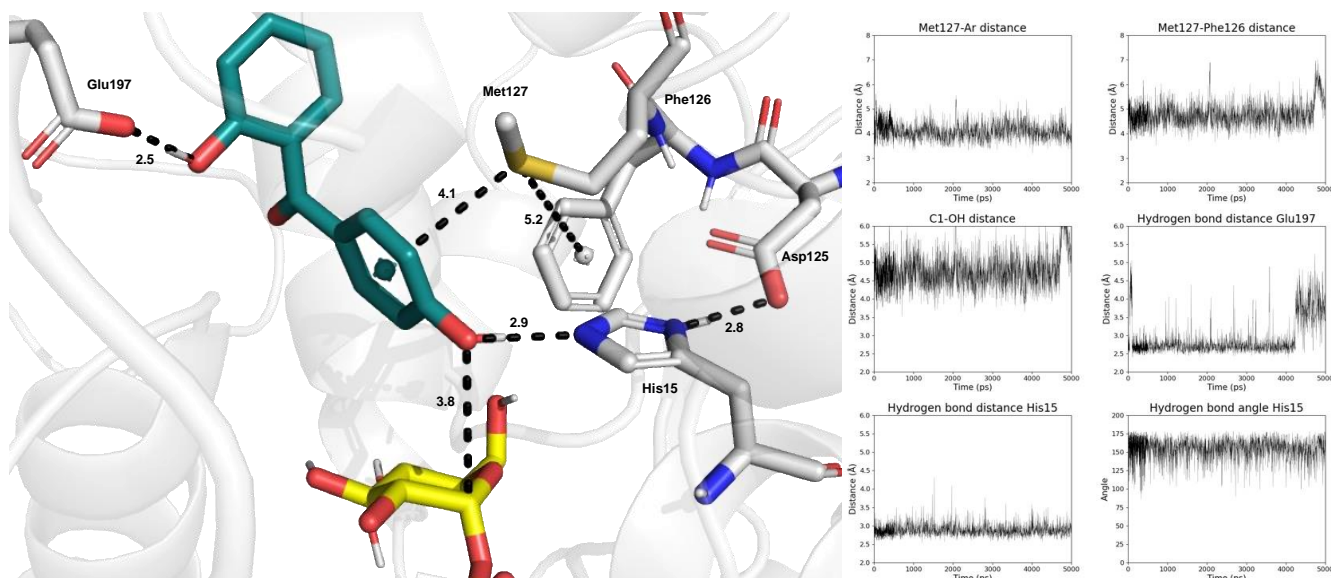


Figure 3. Molecular simulation of the ternary Michaelis complex in the presence of UDP-Glc and 2,4'-dihydroxybenzophenone. Left, minimized ternary complex showing key interactions showing 2,4'-dihydroxybenzophenone (cyan), UDP-glucose (yellow), and interacting residues (white). Right, monitoring of selected distances and angles from MD trajectories.

Clearly, Met127 appeared to be a key residue within the active site of *GmUGT88E3* and is absent from the other 39 GT1s assayed. Therefore, five mutants were constructed to verify the significance of Met127 in substrate binding and regioselectivity. However, M127A, M127L, M127I, and M127E could not be purified, possibly due to the disruption of the methionine-aromatic bridging motif between Phe126 and Met127. Only M127K, which was chosen as it might present a replacement stabilizing cation- π interaction, was successfully purified and found active (Figure S10).^{16,23} However, the activity was drastically reduced compared to the wild-type enzyme, leading to severely reduced yields even at 10-fold higher enzyme loadings (Fig. 4). This large difference in activity clearly demonstrates how the loss of the Met127 is detrimental to activity. Note that methionines are most commonly substituted by I, L, or K.²²

To summarize, the potent *GmUGT88E3* was identified as a particularly interesting biocatalyst, being able to deliver high product yields (>90%) and perfect regioselectivity for a broad substrate range of polyphenol glucosylation. A substrate panel was established based on observed regioselectivity, kinetic values and chemical structures were determined. A fast NMR methodology to determine the structure of the products directly from the enzymatic mixture was established via 1D NOESY experiments. Strikingly, the molecular determinant that governs selectivity appears to be a Met-Ar bridge, leading to a Phe126-Met127-phenol interaction.

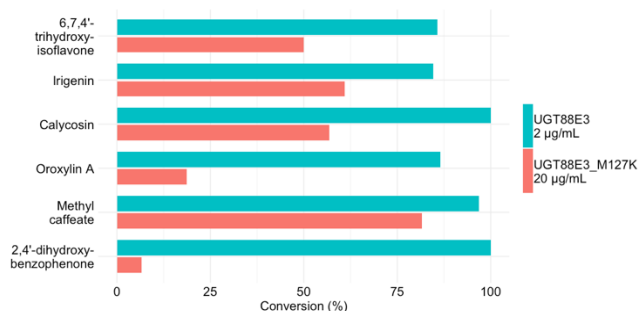


Figure 4. Comparison of *GmUGT88E3* wild-type (2 µg/mL) and mutant *GmUGT88E3_M127K* (20 µg/mL) against 6 of the assessed aglycones. The reactions were monitored by HPLC after 90 min at 25°C in Na-phosphate buffer pH 8. Similar results after 30 min are displayed in Fig. S18.

ASSOCIATED CONTENT

Supporting Information

Michaelis-Menten plots, representative HPLC chromatograms, supporting figures for glycoside structure as determined by NMR, supporting figures for active site analysis with MD data, and additional experimental details, materials and methods (PDF).

Accession Codes

GmUGT88E3 – UniprotKB: A6BM07, GenBank: AB292164.1

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Notes

The authors declare no competing financial interests.

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